BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

J01749:Cloning vector pBR322, complete sequence

Results for: gb|J01749.1 Cloning vector pBR322, complete sequence(4361bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
        gi|208958|gb|J01749.1|SYNPBR322
Description
        Cloning vector pBR322, complete sequence
Molecule type
        nucleic acid
Query Length
        4361

Subject ID
        gi|335823|gb|J02425.1|VACTKN
Description
        vaccinia virus thymidine kinase gene and flanks
Molecule type
        nucleic acid
Subject Length
        794
Program
        BLASTN 2.2.19+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Karlin-Altschul statistics

| Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Graphic Summary

Distribution of 10 Blast Hits on the Query Sequence

?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.
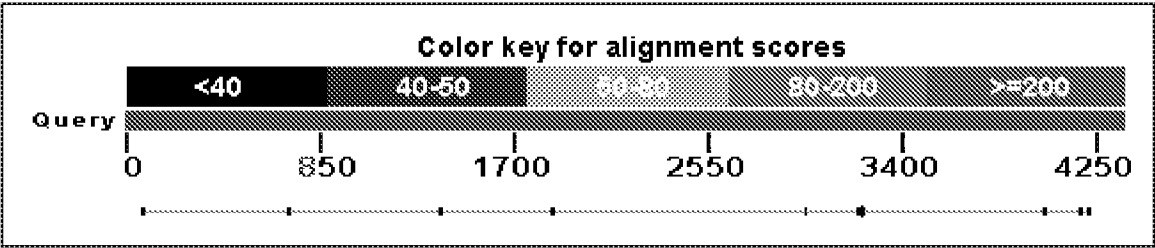
Plot of gi|208958|gb|J01749.1|SYNPBR322 vs gi|335823|gb|J02425.1|VACTKN [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: ▣ UniGene ▣ GEO ▣ Gene ▣ Structure ▣ Map Viewer

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Sequences producing significant alignments:
(Click headers to sort columns)
J02425.1  vaccinia virus thymidine kinase gene and flanks       22.9  200   3%    0.42  100%
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>gb|J02425.1|VACTKN   vaccinia virus thymidine kinase gene and flanks
Length=794

Sort alignments for this subject sequ
  E value   Score   Percent identity
  Query start position   Subject start

 Score = 22.9 bits (24),   Expect = 0.42
 Identities = 15/17 (88%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 4168   AATATTATTGAAGCATT   4184
              |||| | ||||||||||
Sbjct 390   AATAATTTTGAAGCATT   406

 Score = 21.1 bits (22),   Expect = 1.5
 Identities = 14/16 (87%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query 1378   AACATATCCATCGCGT   1393
              || |||||||||| |||
Sbjct 181   AATATATCCATCACGT   166

 Score = 21.1 bits (22),   Expect = 1.5
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 82   GTGTATGAAAT   92
             |||||||||||
Sbjct 635   GTGTATGAAAT   645

 Score = 19.3 bits (20),   Expect = 5.2
 Identities = 16/20 (80%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query 4205   GAGCGGATACATATTTGAAT   4224
              |||| |||| | | ||||||||
Sbjct 102   GAGAGGATTCTTTTTTGAAT   83

 Score = 19.3 bits (20),   Expect = 5.2
 Identities = 13/15 (86%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 3222   TAGATCCTTTTAAAT   3236
              ||||||||| ||| ||
Sbjct 118   TAGATCCTGTTAGAT   132

 Score = 19.3 bits (20),   Expect = 5.2
 Identities = 13/15 (86%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 3202   TATCAAAAAGGATCT   3216
              |||| || ||||||||
Sbjct 133   TATCTAACAGGATCT   119

 Score = 19.3 bits (20),   Expect = 5.2
 Identities = 10/10 (100%), Gaps = 0/10 (0%)

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  Strand=Plus/Plus

Query  2971   GAAGGACAGT   2980
              ||||||||||
Sbjct  471    GAAGGACAGT   480


 Score = 19.3 bits (20),  Expect = 5.2
 Identities = 13/15 (86%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  715   TATCGTCGCCGCACT   729
             ||| || ||||||||
Sbjct  536   TATAGTAGCCGCACT   550


 Score = 19.3 bits (20),  Expect = 5.2
 Identities = 12/13 (92%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1869   TATCATTACCCCC   1881
              |||||||||| ||
Sbjct  717    TATCATTACCTCC   705


 Score = 19.3 bits (20),  Expect = 5.2
 Identities = 10/10 (100%), Gaps = 0/10 (0%)
 Strand=Plus/Minus

Query  4017   TCGATGTAAC   4026
              ||||||||||
Sbjct  751    TCGATGTAAC   742
```

Select All Get selected sequences Distance tree of results